

Table S4. Two-group significance analysis of microarrays (SAM) between monocytes from patients with metastatic breast cancer (MBC) and sepsis [MBC / Sepsis] compared to monocytes from healthy controls [HC] (excluding tuberculosis patients and the breast cancer patient that clustered with healthy controls). The table specifies the 126 genes with significantly higher expression in [MBC / sepsis] as compared to HC (FDR < 0.05) and relevant pathways as identified by gene ontology (DAVID). Genes in bold are the 37 significantly differentially expressed genes (SAM, FDR<0.05) between 1) monocytes from patients with [MBC / sepsis] and 2) monocytes from [HC / tuberculosis]. Genes of special interest in MDSCs and monocyte reprogramming are highlighted in red.

Gene expression higher in [MBC / sepsis] as compared to HC			
Cluster	Gene symbol	GO term	P-value
Grey	HBB, HBA1, HBA2, IFIT3, ZBP1, LOC643332, ETS1, CCDC109A, C3AR1, SAMSN1, BCL2A1, MIR1974 , MS4A4A, E2F2, LOC391769, BATF, TMEM70, RNASE3 , TNFAIP8L2, MLSTD1, PPIG, FBXO38, FPRL1, C1orf25, RNASEL, ST8SIA4, KBTBD7, CEBPE, PPP2R2A, RRM2B, DHRS9, NRBF2, ANKRD22, NKG7 , S100A12, NFE2, LOC100129243, ADCY3, FADD, AMY1B, ST8SIA4, MFAP1, SP3, WDR44, RAB33B, CRSP3, NLRC4, LOC728006, TLR8, GPR30	GO:0006952~defense response	5.9E-4
		GO:0042742~defense response to bacterium	0.003
		GO:0009617~response to bacterium	0.01
Red	OLFM4 , CHI3L1 , CAMP, LOC653600 , LOC728358 , DEFA3, DEFA1, PGLYRP1 , CEACAM8 , CD24 , LCN2 , TCN1 , CEACAM1 , CLC, TLR1, TFF3 , OLR1 , LTF, MYB, ATP8B4	disulfide bond	1.1E-7
		GO:0005576~extracellular region	1.1E-6
		GO:0006952~defense response	1.6E-7
		GO:0009617~response to bacterium	2.2E-6
Dark blue	RETN, STOM, GPR84, NUSAP1, TSPAN2, CTSG , ELA2 , DEFA4 , MPO , CEACAM6 , BPI , AZU1 , DACH1, CYP4F3 , ANXA3 , MS4A3 , COL17A1 , HP, ORM1, RNF24, CST7 , LRG1, MMP25 , MMP9 , ARG1 , S100P , IL18RAP , CA4 , Rgr , C5orf32, ALOX5AP, IFITM1, TNFAIP6 , AQP9, ACSL1, SLC26A8, VNN1, N4BP1, HLX1, B4GALT5, TTRAP, RNF149, C7orf25, ZNF398, ALPK1, ACTN1, DYSF, ASF1B	GO:0006952~defense response	8.6E-6
		GO:0006954~inflammatory response	0.003
		GO:0009611~response to wounding	0.004
		disulfide bond	9.6E-5
		antibiotic	6.1E-4